



Genetic variability, divergence, correlation and path analysis in okra (*Abelmoschus esculentus*) for yield improvement

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ABSTRACT

Genetic variability and trait association analyses are crucial for effective parent selection in okra [*Abelmoschus esculentus* (L.) Moench] breeding programme. However, the lack of integrated information on variability, divergence, and yield-related traits often limits precision in breeding decisions. To address this, the present study evaluated 25 okra genotypes along with ‘Punjab-8’ as a standard check during 2022 and 2023 at College of Horticulture and Forestry, Neri, Himachal Pradesh. The experiment was laid out in a randomised complete block design (RCBD) having three replications. Data on growth, yield, and quality traits were recorded and pooled analyses were conducted to estimate variability, correlations, path coefficients, principal component analysis and genetic divergence. Substantial variability was observed among genotypes for most traits. The genotype COHF N-2 was notable for early flowering, taller plants, and superior fruit weight and yield/plant. High phenotypic and genotypic coefficients of variation were recorded for mucilage content, first flowering node, and fruit yield/plant. Most traits exhibited high heritability, suggesting that phenotypic selection would be effective. Correlation analysis indicated that pod number/plant and pod weight were positively associated with yield, while path coefficient analysis revealed a strong direct effect of seeds/pod on yield. Genetic divergence grouped the genotypes into four distinct clusters. The diverse and superior genotypes identified in this study can be effectively utilised in breeding programmes aimed at yield improvement in okra.

Keywords: Principal component analysis, Path coefficient analysis, Yield components

Okra [*Abelmoschus esculentus* (L.) Moench] under the family Malvaceae is widely recognised as one of the most nutrient-rich vegetable crops cultivated in India (Temam *et al.* 2021). Okra, is known to be allopolyploid, exhibits a consistent pattern of polyploidy, with reported somatic chromosome count of $2n=72, 109, 120, 132$ and 144 (Raghuwanshi *et al.* 2025). India leads the world in okra cultivation and production, contributing approximately 72% overall. The country cultivates okra on 554 thousand ha, yielding 7,289 thousand tonnes of tender fruits annually, with a productivity rate of 13.15 t/ha. In Himachal Pradesh, okra is grown on 3.65 thousand ha, producing 70.24 thousand tonnes annually and achieving a productivity of 19.24 t/ha (Indiastat 2024). The occurrence of crossbreeding, ranging from 4–19%, with a peak of 42.2%, is observed through insect-facilitated pollination (Yawalkar 1965, Fufa 2019).

The success of any crop improvement programme largely depends on the magnitude of genetic variability, heritability, and the nature of association among yield and its component traits. Understanding the extent of genetic variation in available germplasm is essential for the effective selection of desirable genotypes and for developing superior recombinants (Temam *et al.* 2021, Behera 2025). Although okra has significant inherent productivity potential, its yield has been declining, and average productivity remains insufficient due to inadequate utilisation of available genetic resources and lack of well-defined selection criteria (Ranga and Darvhankar 2022). Evaluation of germplasm for genetic divergence and trait association is therefore crucial for identifying genetically diverse parents and improving selection efficiency in breeding programmes (Syfullah *et al.* 2024). The Mahalanobis D^2 statistic is a widely used multivariate approach for assessing genetic divergence based on quantitative traits and aids in the identification of suitable parents for hybridisation (Osekita and Atimokhale 2024). Despite numerous studies on genetic variability in okra, limited efforts have integrated multivariate approaches such as principal component analysis and path coefficient analysis to identify key yield-

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contributing traits and translate them into practical breeding strategies. Furthermore, the biological interpretation of trait associations in relation to yield improvement remains insufficient. Therefore, the present study was undertaken to evaluate genetic variability, trait association, and genetic divergence among okra genotypes using multivariate approaches, with the objective of identifying key selection criteria for yield improvement.

MATERIALS AND METHODS

The present study was carried out during the spring-summer seasons of 2022 and 2023 at College of Horticulture and Forestry, Neri (30°52'30"N, 77°11'30"E; at an elevation of 1,276 m amsl), Himachal Pradesh. Twenty-five genotypes were collected from several resources and compared with the standard variety 'P-8' (check variety) (Table 1). The experiment was laid out in a randomised complete block design (RCBD) with three replications. Each genotype was grown in plots of size 2.4 m × 2.0 m, maintaining a spacing of 60 cm × 20 cm between rows and plants, respectively. Standard agronomic practices, including recommended doses of fertilisers, irrigation, weeding, and plant protection measures were uniformly followed for all treatments throughout the crop growth period. Fruit traits were recorded from five representative plants for each genotype within every replication, and the mean values obtained were subjected to statistical analysis. All genotypes were evaluated for the following traits: First fruiting node; Days to 50% flowering, Internodal length (cm); Leaf length (cm); Leaf width (cm); Ridges/fruit; pods/plant; pod diameter (cm); pod length (cm); pod weight (g); Seeds/pod; 100-seed weight (g); Plant height (cm); Dry matter content (%); Mucilage content (g); Total soluble solids (°B); Ascorbic acid (mg) and Pod yield/plant (g).

Statistical analysis: The pooled data collected from two years, i.e. 2022 and 2023 was analysed using MS-Excel, OP-STAT, TNAU-STAT and PAST software. The average values obtained for each genotype across replications covering all traits under investigation were analysed statistically using a randomised complete block design (RCBD).

Analysis of variance: The collected data from two years on various quantitative traits were pooled and analysed for variance using the method described by Panse and Sukhatme (1967). The coefficient of variability was calculated using formula provided by Burton and Devane (1953), heritability by Hanson *et al.* (1956), genetic advance by Johnson *et al.* (1955) and genetic gain by Warshamana (2005). The correlations among studied traits at the genotypic, phenotypic and environmental levels were estimated using the procedure outlined by Al-Jibouri *et al.* (1958). The path coefficient study was calculated by using the formula provided by Dewey and Lu (1959). Principal component analysis (PCA) was applied, following the method of Abdi and Williams (2010) to determine the major sources of variation among the genotypes. The Mahalanobis D²

Table 1 List of okra genotypes along with their sources of collection

Genotypes	Source
COHF N-1	College of Horticulture and Forestry, Neri, Himachal Pradesh
COHF N-2	College of Horticulture and Forestry, Neri, Himachal Pradesh
COHF N-3	College of Horticulture and Forestry, Neri, Himachal Pradesh
COHF N-4	College of Horticulture and Forestry, Neri, Himachal Pradesh
COHF N-5	College of Horticulture and Forestry, Neri, Himachal Pradesh
COHF N-7	College of Horticulture and Forestry, Neri, Himachal Pradesh
COHF N-14	College of Horticulture and Forestry, Neri, Himachal Pradesh
COHF N-15	College of Horticulture and Forestry, Neri, Himachal Pradesh
COHF N-16	College of Horticulture and Forestry, Neri, Himachal Pradesh
UHF-Okra-2	Dr Y S Parmar University of Horticulture and Forestry, Solan, Himachal Pradesh
UHF-Okra-4	Dr Y S Parmar University of Horticulture and Forestry, Solan, Himachal Pradesh
Kashi Vibhuti	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Kashi Mahima	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Kashi Pragati	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Kashi Satdhari	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Kashi Chaman	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Kashi Mangla	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Kashi Kranti	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh
Jammu Okra 5	Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu
Hisar Unnat	Chaudhary Charan Singh Hisar Agricultural University, Haryana
Hisar Naveen	Chaudhary Charan Singh Hisar Agricultural University, Haryana
Varsha Uphar	Chaudhary Charan Singh Hisar Agricultural University, Haryana
Palam Komal	Chaudhary Sarwan Kumar Himachal Pradesh Agriculture University
Pb. Suhabani	Punjab Agricultural University, Ludhiana, Punjab
P-8 (check variety)	Punjab Agricultural University, Ludhiana, Punjab

statistics, as suggested by Rao (1972), were employed to assess genetic divergence.

RESULTS AND DISCUSSION

Variability studies: The study of variability among different traits in okra genotypes was performed using Bartlett's chi-square test, which was applied to evaluate the goodness of fit and the homogeneity of variances. As Bartlett's test was found to be insignificant for the *khari*f seasons of 2022 and 2023, the data for these two seasons were pooled together and further analysed.

Phenotypic and genotypic coefficient of variation: The Phenotypic Coefficients of Variation (PCV) values were higher than the Genotypic Coefficients of Variation (GCV) values, though they were relatively close (Table 2), indicating that environmental effects were present but had minimal impact on the traits expression. Moderate variability (i.e. 15–30 %) was recorded for traits such as mucilage content, first fruiting node, pod yield/plant, seeds/pod, internodal length and number of pods/plant and these results were in align with the research conducted by Kumar *et al.* (2021), Mohammed *et al.* (2022a;b) and

Kumar *et al.* (2023). The close alignment between PCV and GCV for these traits indicates that their expression is largely under genetic control, making them dependable targets for selection in breeding programmes. In contrast, the remaining traits exhibited low variability (<15%), reflecting a restricted genetic base and limited potential for improvement through direct selection. Comparable patterns of variability in okra have also been documented by Mishra *et al.* (2024) and Joshi *et al.* (2025) reinforcing the consistency of these findings across different studies.

Heritability and genetic advance: The estimates of heritability coupled with genetic advance revealed substantial genetic control for most of the traits studied (Table 2). Pod yield/plant exhibited high heritability (92.06%) along with high genetic advance (89.99%), indicating the predominance of additive gene action and suggesting that direct selection for this trait would be highly effective in improving yield. Similarly, plant height showed high heritability but moderate genetic advance, implying the involvement of both additive and non-additive gene effects and indicating that selection may be moderately effective. Leaf width showed low heritability, indicating strong

Table 2 Pooled estimation of the PCV, GCV, h^2 , GA, GAM, PC-1, 2, 3

Traits	Mean	Range	h^2	GCV	PCV	GA	GAM	PC1	PC2	PC3
First flowering node	4.65	2.99–6.65	98.81	22.48	22.61	2.14	46.03	0.26	-0.002	-0.011
Days to 50% flowering	48.86	39.50–61.65	96.91	13.81	14.02	13.68	28.00	0.175	-0.258	0.316
Internodal length (cm)	9.74	7.07–13.54	97.7	17.62	17.82	3.49	35.88	0.282	0.124	-0.032
Leaf length	23.48	19.54–26.48	91.24	7.77	8.14	3.59	15.30	-0.239	0.297	-0.137
Leaf width	34.14	31.50–37.16	64.79	3.49	4.34	1.97	5.79	-0.215	0.412	0.197
Ridges/fruit	5.24	5.00–7.00	95.17	11.00	11.28	1.15	22.11	0.004	0.194	0.752
Pods/plant	16.36	12.42–23.54	97.76	17.29	17.48	5.76	35.21	-0.239	0.09	0.09
Pod diameter (cm)	1.52	1.16–1.89	93.95	9.31	9.61	0.28	18.59	-0.286	-0.121	-0.081
Pod length (cm)	12.21	10.36–13.55	84.84	6.61	7.18	1.53	12.55	-0.259	-0.145	0.174
Pod weight (g)	12.70	10.85–15.05	92.74	9.58	9.94	2.42	19.00	-0.191	-0.275	-0.16
Seeds/pod	59.51	45.65–92.54	98.51	18.59	18.73	22.62	38.01	-0.28	0.012	-0.117
100-seed weight (g)	6.01	4.04–7.08	95.72	11.70	11.96	1.41	23.58	0.016	0.628	-0.29
Plant height (cm)	143.26	99.19–168.45	96.5	13.43	13.67	38.94	27.18	-0.257	-0.191	0.011
Dry matter content (%)	14.15	11.65–17.98	96.75	14.03	14.27	4.02	28.44	-0.22	0.1	-0.051
Mucilage content (g)	0.36	0.13–0.54	98.62	23.55	23.72	0.17	48.19	-0.266	-0.057	0.177
Total soluble solids (°B)	6.96	6.04–7.71	85.52	6.93	7.5	0.92	13.21	-0.267	-0.121	-0.119
Ascorbic acid (mg/100 g)	10.72	9.01–11.88	87.76	7.61	8.13	1.57	14.70	-0.232	0.186	0.242
Pod yield/plant (g)	204.43	130.85–310.10	92.06	21.58	21.79	89.99	44.02	-0.296	-0.097	-0.036
Eigen values								10.63	1.889	1.337
Variation								0.591	0.105	0.074
Cumulative variation								0.591	0.696	0.77

PCV, Phenotypic coefficient of variation; GCV, Genotypic coefficient of variation; h^2 , Heritability; GA, Genetic advance; GAM, Genetic advance mean; PC, Principal component.

environmental influence and limited potential for direct selection. Therefore, improvement may be more effective through indirect selection using correlated traits with higher heritability. Overall, traits expressing high heritability in association with high or moderate genetic advance can serve as reliable selection criteria, as their improvement is less influenced by environmental factors. Comparable findings have also been reported in okra by Kumar *et al.* (2023), Mishra *et al.* (2024), Behera *et al.* (2025) and Appiah *et al.* (2026) for yield and related traits.

Correlation studies: The pooled analysis over two years revealed that pod yield/plant was positively and significantly associated with key growth, yield, and quality traits while, earliness-related traits exhibited a significant negative association with yield, indicating that delayed flowering and increased vegetative spacing may adversely affect productivity (Table 3). Seeds/pod showed a strong positive correlation with pod yield/plant ($r = 0.944$). This indicates its major role in determining yield and highlights it as a reliable trait for selection in okra breeding programmes. The calculation of correlation studies revealed that important yield related traits like pod size and number of pods/plant play a crucial role in enhancing overall productivity, suggesting their importance as selection indices in breeding programmes. These relationships indicate that simultaneous improvement of these positively associated traits can lead to indirect selection gains in yield. The correlation biplot (Supplementary Fig. 1) further supports these associations by visually depicting the positive (red colour) and negative (yellow colour) relationships among the studied traits. Kumar *et al.* (2018), Kumar *et al.* (2023), Abdalla *et al.* (2025) and Behera *et al.* (2025) also recorded similar trend for correlation studies for most of the traits.

Path analysis: The results through the pooled analysis for path analysis revealed that seeds/pod exhibited the maximum positive and direct effects on pod yield/plant that is further followed by traits namely plant height, total soluble solids, mucilage content, pod weight, leaf length, ridges/fruit, dry matter content and pod length (Table 4). However, first fruiting node showed maximum negative direct impact on pod yield/plant that is followed by internodal length, seed weight, pods/plant, days to 50% flowering, ascorbic acid and leaf width. The strong positive direct effect of seeds/pod on yield indicates that reproductive efficiency plays a crucial role in determining overall productivity, as higher seed number reflects better fertilisation success and resource allocation towards sink development. Similarly, pod weight and pod length contributed positively to yield, suggesting that larger and heavier pods directly enhance marketable yield and are important selection criteria in breeding programmes. Plant height showed a positive direct effect, which may be attributed to its association with increased vegetative growth and photosynthetic capacity, thereby supporting higher assimilate production and translocation to developing pods. Behera *et al.* (2025) and Singh *et al.* (2025) also recorded significantly positive results for the plant height. Traits

such as total soluble solids and mucilage content, although primarily quality parameters, also exhibited positive direct effects, indicating their possible linkage with metabolic efficiency and overall plant vigour.

Similarly, traits like internodal length and days to 50% flowering showed negative direct effects, indicating that delayed flowering and excessive vegetative elongation might adversely affect yield by reducing reproductive efficiency and timely pod development. Awasthi *et al.* (2022) and Vennila *et al.* (2026) also observed negative direct effects for traits responsible for earliness. Meanwhile, maximum positive indirect effect of pod diameter was observed via seeds/pod on pod yield/plant. This indicates that although pod diameter has a negative direct effect (-0.131), it showed a strong and significant positive genotypic correlation with yield ($r_g = 0.906$). This positive association was mainly attributable to favourable indirect effects through seeds/pod, plant height, mucilage content and total soluble solids. The results were in align with the findings of Joshi *et al.* (2025) and Singh *et al.* (2025). In the present study, the residual effect of 0.0345 was observed, which is very low and indicates that the majority of yield variation has been effectively explained by the traits included in the analysis, confirming the reliability of the path model. The positive direct effect of pod weight on pod yield/plant and negative direct effect of internodal length on pod yield/plant were also reported by Kumar *et al.* (2023). Patel *et al.* (2019) also observed positive direct effects of pod length and pod weight on pod yield/plant, whereas negative direct effects of days to 50% flowering and pod diameter on pod yield/plant.

Principal component analysis: Higher absolute values of Principal Component Analysis (PCA) suggested stronger influence (Supplementary Table 2, Supplementary Fig. 2). The results revealed that for PC1, traits like internode length (0.282), pod yield (-0.296), pod diameter (-0.286), and first fruiting node (0.26) have strong contributions while for PC2, traits like seed weight (0.628), leaf width (0.412), and days to 50 % flowering (-0.258) were significant. Meanwhile for PC3, traits like ridges on fruit (0.752) and days to 50% flowering (0.316) showed strong contributions. Together, the first three principal components explained 77% of the total variance in data where PC1 accounts for 59.1% PC2 for 10%, and PC3 for 7% of the total variance. The high contribution of PC1 indicated that traits associated with plant growth and yield components, such as internodal length, pod diameter, and first fruiting node play a major role in determining overall variability and productivity in okra genotypes. Traits loading heavily in PC1, particularly pod yield and pod diameter, directly influenced yield by affecting sink size and resource allocation, whereas first fruiting node and internodal length influenced earliness and plant growth, which in turn determine the efficiency of assimilate partitioning towards reproductive organs. In PC2, the high contribution of seed weight and leaf width suggests the importance of seed development and photosynthetic surface area in influencing

Table 3 Genotypic coefficient of correlation for several horticultural traits in okra (Pooled data)

Traits	FN	DF	IL	LL	LW	RF	PP	PD	PL	PW	SP	SW	PH	DM	MC	TS	AA	PY
FN	1.000																	
DF	0.556*	1.000																
IL	0.788*	0.453*	1.000															
LL	-0.596*	-0.540*	-0.647*	1.000														
LW	-0.551*	-0.424*	-0.580*	0.804*	1.000													
RF	-0.064	0.054	0.043	-0.093	0.300	1.000**												
PP	-0.606*	-0.316	-0.657*	0.612*	0.660*	0.021	1.000											
PD	-0.735*	-0.552*	-0.820*	0.674*	0.534*	-0.093	0.701*	1.000										
PL	-0.725*	-0.277	-0.837*	0.548*	0.515*	0.077	0.611*	0.780*	1.000									
PW	-0.516*	-0.290	-0.590*	0.371	0.247	-0.115	0.368	0.733*	0.561*	1.000								
SP	-0.781*	-0.551*	-0.808*	0.657*	0.613*	-0.123	0.797*	0.852*	0.717*	0.534*	1.000							
SW	0.057	-0.359	0.192	0.307	0.322	-0.029	0.045	-0.148	-0.221	-0.222	0.023	1.000						
PH	-0.647*	-0.447*	-0.812*	0.541*	0.393	-0.080	0.597*	0.844*	0.674*	0.564*	0.714*	-0.242	1.000					
DM	-0.612*	-0.270	-0.605*	0.654*	0.662*	-0.090	0.500*	0.636*	0.582*	0.507*	0.631*	0.036	0.437*	1.000				
MC	-0.614*	-0.398*	-0.854*	0.660*	0.603*	0.097	0.753*	0.848*	0.745*	0.459*	0.743*	-0.162	0.829*	0.468*	1.000			
TS	-0.766*	-0.524*	-0.815*	0.630*	0.430*	-0.162	0.566*	0.821*	0.771*	0.516*	0.804*	-0.164	0.733*	0.595*	0.668*	1.000		
AA	-0.628*	-0.442*	-0.609*	0.609*	0.636*	0.241	0.557*	0.610*	0.645*	0.209	0.616*	0.085	0.672*	0.597*	0.652*	0.662*	1.000	
PY	-0.842*	-0.541*	-0.916*	0.666*	0.574*	-0.063	0.735*	0.906*	0.809*	0.627*	0.944*	-0.143	0.841*	0.633*	0.829*	0.887*	0.677*	1.000

*Significant at 0.05% level. FN, First fruiting node; DF, Days to 50% flowering; IL, Internodal length; LL, Leaf length; LW, Leaf width; RF, Ridges on fruit; PP, Pods/plant, PD, Pod diameter; PL, Pod length; PW, Pod weight; SP, Seeds/pod; SW, Seed weight; PH, Plant height; DM, Dry matter content; MC, Mucilage content; TS, Total soluble solids; AA, Ascorbic acid; PY, Pod yield/plant.

Table 4 Path analysis (direct and indirect effects) for several horticultural traits in okra (Pooled data)

Traits	FN	DF	IL	LL	LW	RF	PP	PD	PL	PW	SP	SW	PH	DM	MC	TSS	AA	PY (r_g)
FN	-0.113	-0.013	-0.077	-0.021	0.009	-0.002	0.034	0.094	-0.003	-0.036	-0.423	-0.003	-0.095	-0.014	-0.079	-0.100	0.009	-0.842*
DF	-0.062	-0.024	-0.044	-0.019	0.007	0.002	0.018	0.070	-0.001	-0.020	-0.297	0.022	-0.065	-0.006	-0.051	-0.068	0.006	-0.541*
IL	-0.088	-0.010	-0.099	-0.022	0.009	0.001	0.037	0.105	-0.004	-0.042	-0.438	-0.012	-0.119	-0.013	-0.110	-0.107	0.009	-0.916*
LL	0.065	0.012	0.061	0.036	-0.012	-0.003	-0.034	-0.083	0.002	0.025	0.348	-0.018	0.077	0.014	0.083	0.080	-0.008	0.666*
LW	0.055	0.009	0.049	0.023	-0.018	0.008	-0.032	-0.060	0.002	0.014	0.298	-0.016	0.050	0.014	0.068	0.051	-0.008	0.574*
RF	0.007	-0.001	-0.004	-0.003	-0.005	0.031	-0.001	0.010	0.000	-0.008	-0.066	0.002	-0.012	-0.002	0.014	-0.020	-0.003	-0.063
PP	0.068	0.007	0.064	0.021	-0.010	0.001	-0.057	-0.090	0.003	0.026	0.431	-0.003	0.087	0.011	0.098	0.073	-0.008	0.735*
PD	0.081	0.013	0.079	0.023	-0.008	-0.002	-0.039	-0.131	0.004	0.051	0.456	0.009	0.122	0.014	0.107	0.107	-0.008	0.906*
PL	0.078	0.006	0.078	0.017	-0.008	0.002	-0.033	-0.095	0.005	0.037	0.370	0.012	0.095	0.012	0.092	0.095	-0.009	0.809*
PW	0.056	0.007	0.057	0.012	-0.003	-0.003	-0.020	-0.092	0.003	0.073	0.286	0.013	0.081	0.011	0.058	0.066	-0.003	0.627*
SP	0.087	0.013	0.079	0.023	-0.010	-0.004	-0.045	-0.109	0.003	0.038	0.548	-0.001	0.104	0.014	0.095	0.105	-0.009	0.944*
SW	-0.006	0.008	-0.019	0.010	-0.005	-0.001	-0.003	0.018	-0.001	-0.016	0.013	-0.062	-0.034	0.001	-0.020	-0.022	-0.001	-0.143
PH	0.072	0.010	0.079	0.018	-0.006	-0.002	-0.033	-0.108	0.003	0.040	0.384	0.014	0.149	0.010	0.107	0.097	-0.009	0.841*
DM	0.069	0.006	0.059	0.022	-0.011	-0.003	-0.028	-0.081	0.003	0.035	0.341	-0.002	0.063	0.023	0.059	0.077	-0.008	0.633*
MC	0.068	0.009	0.083	0.023	-0.009	0.003	-0.043	-0.107	0.004	0.033	0.399	0.010	0.122	0.010	0.131	0.087	-0.009	0.829*
TSS	0.082	0.012	0.077	0.021	-0.007	-0.004	-0.030	-0.101	0.003	0.035	0.417	0.010	0.104	0.013	0.082	0.138	-0.009	0.887*
AA	0.068	0.010	0.058	0.020	-0.009	0.007	-0.031	-0.075	0.003	0.014	0.323	-0.005	0.096	0.013	0.082	0.083	-0.015	0.677*

*Significant at 0.05% level. Residual effect = 0.0345, r_g . Genotypic coefficient of correlation; Bold values presented diagonally are direct effects. FN, First fruiting node; DF, Days to 50% flowering; IL, Internodal length; LL, Leaf length; LW, Leaf width; RF, Ridges on fruit; PP, Pods/plant; PD, Pod diameter; PL, Pod length; PW, Pod weight; SP, Seeds/pod; SW, Seed weight; PH, Plant height; DM, Dry matter content; MC, Mucilage content; TS, Total soluble solids; AA, Ascorbic acid; PY, Pod yield/plant.

yield potential. Larger leaf area enhances photosynthetic efficiency, thereby increasing assimilate production, while higher seed weight reflects better resource accumulation within reproductive structures. Similarly, in PC3, the strong contribution of ridges on fruit and days to 50% flowering indicates their role in morphological differentiation and crop duration, which can indirectly affect yield through their influence on fruit development and maturity period. Early or optimal flowering ensures better synchronisation with environmental conditions, ultimately improving yield performance. Overall, the PCA results indicate that both yield-contributing traits (such as pod yield, seed weight, and pod diameter) and supporting traits (such as leaf width, flowering time, and plant architecture) collectively influence productivity through their effects on growth, photosynthesis, and assimilate partitioning. Therefore, these traits should be given priority in selection and hybridisation programmes aimed at yield improvement. This analysis highlights the key traits that contribute to genetic variability and can inform further studies and breeding programmes. Kumar *et al.* (2023), Joy *et al.* (2026) and Vennila *et al.* (2026) also recorded similar results for principal component analysis.

Genetic divergence analysis: The clustering of genotypes into four groups based on morphological differences, along with the greater inter-cluster distance compared to intra-cluster distance, indicated a high level of heterogeneity among the various genotypes and is depicted via a Dendrogram (Supplementary Fig. 3). The 25 genotypes were grouped into four clusters, where clusters I (11) and IV (11) contained the maximum number of genotypes, followed by cluster II (2) and cluster III (1). The maximum inter-cluster distance of 124.88 was observed between clusters II and III, while the minimum inter-cluster distance of 45.82 was observed between clusters I and IV. Therefore, promising genotypes with the greatest inter-cluster distance can be used as parents in future breeding programmes to produce superior heterotic segregants. Cluster II showed the maximum intra-cluster distance value of 30.43, whereas cluster III had the minimum value of 0.00 (Table 5). Due to the low probability of diverse populations emerging from hybridisation within the same cluster, it is advantageous to use genotypes from different clusters for breeding purposes.

The average mean values of all the 25 genotypes in the four clusters showed that each cluster excelled in different traits (Table 6). Genotypes in cluster II were observed with

desirable mean values for almost all the traits where they reached 50% flowering in just 40.75 days, the shortest duration among all clusters, started fruiting at 3.09 node, had shorter internodal length (7.52 cm) while maximum mean values for traits like leaf length (26.29 cm) and leaf width (36.24 cm), number of pods/plant (23.19), pod diameter (1.79 cm), pod length (13.81 cm), pod weight (13.87 g), seeds/pod (89.05), seed weight (6.65 g), plant height (166.50 cm), dry matter content (17.27%), mucilage content (0.48%), total soluble solids (7.70°B), ascorbic acid (11.83 mg) and pod yield/plant (291.32 g) were observed. However, genotypes in cluster IV recorded maximum mean values for ridges/fruit. The above-mentioned results aligned with the findings concluded by Mohammed *et al.* (2022), Kumar *et al.* (2023) and Sood *et al.* (2025).

Based on overall mean performance, the genotypes, namely Kashi Kranti and COHF N-2 consistently exhibited superior performance for key economic traits across both years, indicating their suitability as potential parents in breeding programmes. These genotypes can be effectively utilised in hybridisation programmes to enhance yield potential and stability. The study highlights the importance

Table 6 Pooled cluster mean values for several growth, fruit, seed, yield and quality traits in okra

Traits	I	II	III	IV
DF	50.40	40.75	61.65	47.62
FN	5.54	3.09	5.23	3.98
IL	11.07	7.52	13.53	8.46
LL	22.87	26.29	19.54	23.92
LW	33.71	36.24	31.50	34.41
RF	5.24	5.00	5.00	5.29
PP	14.98	23.19	12.99	16.78
PD	1.44	1.79	1.16	1.58
PL	11.67	13.81	10.85	13.27
PW	12.17	13.87	10.85	13.27
SP	51.95	89.05	45.65	62.94
SW	6.29	6.65	6.01	5.60
PH	131.97	166.50	99.19	154.31
DM	13.14	17.27	11.65	14.80
MC	0.32	0.48	0.13	0.40
TSS	6.64	7.70	6.03	7.23
AA	10.40	11.83	9.00	10.98
PY	171.17	291.32	130.85	228.57

FN, First fruiting node; DF, Days to 50% flowering; IL, Internodal length; LL, Leaf length; LW, Leaf width; RF, Ridges on fruit; PP, Pods/plant; PD, Pod diameter; PL, Pod length; PW, Pod weight; SP, Seeds/pod; SW, Seed weight; PH, Plant height; DM, Dry matter content; MC, Mucilage content; TSS, Total soluble solids; AA, Ascorbic acid; PY, Pod yield/plant.

Table 5 Inter and intra cluster (D^2 values) analysis of pooled data collected from two years

Cluster	I	II	III	IV
I	28.88	88.10	48.77	45.82
II		30.43	124.88	55.24
III			0.00	79.17
IV				25.12

of integrating variability, divergence and trait association for efficient parent selection and crop improvement. Among the studied traits, seeds/pod exhibited a strong positive association with yield, indicating its major contribution to productivity. Path analysis further confirmed seeds/pod as the most influential trait with a high direct effect on yield. Along with seeds/pod, traits such as pod weight, pod length, and plant height were identified as key yield determinants and can be used as reliable selection criteria. Multivariate analysis revealed that a major proportion of variability was explained by the first few principal components, indicating the contribution of yield-related traits to overall diversity. Genetic divergence analysis grouped the genotypes into distinct clusters, reflecting substantial diversity among the studied material. Therefore, a breeding strategy involving direct selection for high heritable yield-contributing traits combined with hybridisation among genetically diverse genotypes is recommended to develop high-yielding and resilient okra cultivars.

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